

From: [Jay Field](#)
To: [Eric Blischke/R10/USEPA/US@EPA](#)
Cc: [Robert Gensemer](#); [Burt Shephard/R10/USEPA/US@EPA](#); [Joe Goulet/R10/USEPA/US@EPA](#); [Chip Humphrey/R10/USEPA/US@EPA](#); [Robert Neely](#)
Subject: Re: Summary of Sediment Bioassay Interpretation Resolution
Date: 07/14/2009 12:09 PM

Eric et al,

I agree with Bob G's observations. I am in the process of comparing values for the 4 bioassay endpoints and have identified a couple of discrepancies---some appear to be rounding, others related to treatment of the replicates from the R3 tests, and a couple of others that I need to go back to original data. When I finish with this process (hopefully later today), I will distribute the table of values for the 17 reference stations.

one issue with the replicate tox results for G786 and G788: one of the replicate results for 786 did not qualify as reference sample based on the criteria established, but the average of the results did qualify. In my treatment of the reference samples, I averaged the results for each of the control-normalized results for each endpoint for each of the two replicate pairs. I do not recall any specific guidance about treatment of replicates, but I recall raising the issue.

I also support Bob's point about the best fit for 5th pctile, not necessarily the best overall fit. My recommendation is that EPA do the curve-fitting, determine the values, and provide a table of values to use for the thresholds. This would save all of us time and we could move on to more important issues (like what are we going to do with those values).

Jay

Robert Gensemer wrote:

Eric: A few observations from my perspective:

2) The control-normalization looks correct for biomass, but if I recall (I don't have my files with me at the moment) that LWG's biomass values for individual stations did not quite match values that Jay derived for table RE-1.

3) You have the control normalization correct (test/control) but we need to be careful to recommend use of survivorship, not mortality, to be fully consistent with our guidance and numeric examples. I realize Table 2-1 used mortality, but we have been very consistent all along that we need to use survivorship, and from a recent call with Burt, Don McD. agrees that control-normalized survivorship is the correct value to use, not ctrl-norm mortality. Yes, they relate directly (or should I say, inversely) to one another, but the 5th percentile calculation could be different using one vs. the other, so we need to be consistent, and use survivorship.

4) I could not find any explicit guidance regarding the duplicate RE samples. Its not in the McDonald report that I can find, and I don't think we went into this level of detail in the problem formulation. It may be one of those things that just seemed very obvious to all of us, and so never felt the need to explicitly direct it. Actually, it may have only come up, to my recollection, during our own RE calculations in March. So table RE-1 definitely reflects this approach, although I don't think it was spelled out in the text.

6) I agree with your summary here, except to say that we need to not just chose the best overall curve fit, but particularly in the case of Hyalella biomass, we need a curve that fits the lower tail (i.e., 5th %ile) of the distribution best. For the other three endpoints, this is probably not an issue (i.e., best fit is also best 5th %ile fit). But for Hyl biomass, we need to think more carefully about what distribution fits at the lower tail of the distribution. I think this is a valid approach that makes the best out of the available data. LWG's curve

fit created a 5th %ile value that was quite a bit lower than the empirical numbers; I do not think that was the most appropriate representation of the data.

Bob

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 Before printing, please think green.

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Subject: Summary of Sediment Bioassay Interpretation Resolution

As you are aware, we have been discussing some of the details of the LWG's interpretation of the Portland Harbor sediment bioassay results. Some elements of the interpretation were discussed during a conference call on Thursday, June 18, 2009.

Here is where I believe we are:

- 1) No transcription errors were identified during a review of the reference envelope bioassay results.
- 2) The total biomass calculations were done correctly.
- 3) Mortality should be computed as test/control. This is consistent with Table 2-1 in the March 17, 2006 Bioassay Interpretation Report, ASTM Method E-1706, and EPA Guidance.
- 4) Duplicate reference envelope samples should be pooled (averaged) rather than treated as individual samples. This is consistent with February 15, 2008 problem formulation **(Note: is this the correct reference? I could not find this in either the problem formulation nor the MacDonald benthic risk evaluation)**
- 5) Identification of Level 1, Level 2 and Level 3 thresholds: The toxicity thresholds should be calculated based on 10% of the reference envelope not an absolute 10%. This is consistent with Tables RE 1, RE-2 and the text of EPA's March 31, 2009 direction on the Calculation and Use of Reference Envelope for Portland Harbor Sediment Toxicity Test Interpretation
- 6) Identification of the 5% of the reference envelope should be accomplished using a range of curve fitting procedures appropriate for the data set distribution. The curve fitting procedure with the best overall fit should be selected and the 5% calculated using the best fit curve fitting procedure.

The above procedures for computing the results of the bioassay tests, calculating hit/no-hit designations, developing the reference envelope and identifying Level 1, Level 2 and

Level 3 toxicity hits should be followed.

Please look this over and make sure it matches up with the recommended procedures.

See also my note about the pooling of the reference duplicate samples. Once everyone agrees with the outlined procedures, I will send an email to the LWG summarizing this and recommending a conference call to discuss if there area any questions.

Thanks, Eric

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